AMENDMENTS TO THE CLAIMS

This listing of claims replaces all previous versions of claims.

1-36. (Cancelled)

37. (Currently amended) A method of treating a subject having diabetes, comprising administering a gastrin compound ~~according to any of claims 1, 2 and 23~~ comprising: $Z\text{-}Y_m\text{-}X_n\text{-}AA_1\text{-}AA_2\text{-}AA_3\text{-}AA_4\text{-}AA_5\text{-}AA_6$, wherein AA_1 is Tyr or Phe, AA_2 is Gly, Ala, or Ser, AA_3 is Trp, Val, or Ile, AA_4 is Met or Leu, AA_5 is Asp or Glu, and AA_6 is Phe or Tyr the AA_6 being amidated; wherein Z is a polymer which when the polymer is a protein, Z is the amino acid sequence of the protein; Y_m is an optional spacer region comprising m amino acid residues of a small neutral amino acid, and X is selected from any consecutive portions of: residues 1-28 of SEQ ID NO: 1, residues 1-28 of SEQ ID NO: 2, residues 1-11 of SEQ ID NO: 3, and residues 1-11 of SEQ ID NO: 4, providing that the gastrin compound binds a gastrin/CCK receptor.

38. (Original) The method according to claim 37, wherein frequency of administering the gastrin compound is less than frequency of administration of a native gastrin.

39. (Original) The method according to claim 37, further comprising measuring a physiological indicator of islet neogenesis.

40. (Original) The method according to claim 37, further comprising measuring fasting blood glucose (FBG).

41. (Original) The method according to claim 37, further comprising decreasing insulin dependency.

42-47. (Cancelled)

48. (Original) A method of treating a diabetes patient comprising administering to the patient a modified gastrin capable of covalently reacting with a serum protein.

49. (Original) The method according to claim 48, wherein the modified gastrin comprises a sequence of a native gastrin capable of binding to the gastrin/CCK receptor and an amino terminal cysteine or lysine.

50. (Currently amended) The method according to claim ~~42~~ 37, wherein the sequence of the native gastrin is selected from the group of: residues 29-34 of amino acid sequence SEQ ID NO: 1; residues 29-34 of amino acid sequence SEQ ID NO: 2; residues 12-17 of amino acid sequence SEQ ID NO: 3; and residues 12-17 of amino acid sequence SEQ ID NO: 4.

51-53. (Cancelled)

54. (New) A method of claim 37 wherein AA_1-AA_2-AA_3-AA_4-AA_5-AA_6 is Tyr-Gly-Trp-Met-Asp-Phe or Tyr-Gly-Trp-Leu-Asp-Phe.

55. (New) A method according to claim 37, wherein Z is a protein or human serum albumin.

56. (New) A method according to claim 37 wherein Y is a sequence comprising m residues having glycine alternating with alanine or having a random sequence of glycine and alanine.

57. (New) A method according to claim 37 wherein X is selected from the group of sequences: position 1 to position 11 of SEQ ID NO: 3; position 1 to position 11 of SEQ ID NO: 4; position 2 to position 11 of SEQ ID NO: 3; and position 2 to position 11 of SEQ ID NO: 4.

58. (New) A method according to claim 37, further comprising a cysteine residue at the amino terminus of Y when m is greater than 1, or at the amino terminus of X when m is 0.

59. (New) A method according to claim 37 wherein m is 0 to about 20 residues.

60. (New) A method according to claim 37, wherein X_n-AA_1-AA_2-AA_3-AA_4-AA_5-AA_6 further comprises a bifunctional cross-linking agent for linkage to Z if m is 0.

61. (New) A method according to claim 54 wherein the gastrin comprises at least amino acids selected from the group of: positions 29-34 of SEQ ID NO:1; positions 29-34 of SEQ ID NO:2; positions 12-17 of SEQ ID NO: 3; and positions 12-17 of SEQ ID NO: 4, and the gastrin is further associated with a protein, a polymer, a lipid or a carbohydrate.

62. (New) A method of treating a subject having diabetes comprising administering a gastrin compound comprising a structure C-Y_m-X, wherein C is Cys or Lys, Y_m is an optional spacer region comprising m amino acid residues of a small neutral amino acid, and X is at least six amino acid residues comprising sequences selected from at least positions 12-17 of gastrin-17 (SEQ ID NO: 3 and 4) and at least positions 29-34 of gastrin-34 (SEQ ID NO: 1 and 2).